CLAIM AMENDMENTS

1. (previously presented): A method to identify a desired region of a target nucleic acid to be targeted for observation, which method comprises

contacting a sample containing said target nucleic acid and non-target nucleic acid with first and second probes that bracket said region, which first probe comprises a first oligomer specific for a sequence upstream of said region coupled to a first particulate label, and

said second probe comprises a second oligomer specific for a proximal sequence downstream of said region coupled to a second particulate label;

wherein said first and second particulate labels are observable by microscopy, and

observing by microscopy the presence or absence of proximity of the first and second particulate labels to each other, whereby the presence of said proximity identifies said desired region,

wherein said method does not include a step of separating the target nucleic acid from non-target nucleic acid.

2. (currently amended): The method of claim 1, wherein said first and second particulate labels comprise first and second fluorophores.

3. (previously presented): The method of claim 2, wherein said first and second fluorophores are distinguishable from each other.

4. (original): The method of claim 1, wherein said first and second oligomers are peptide nucleic acids.

5. (original): The method of claim 1, wherein said target nucleic acid is single-stranded and said first and second oligomers are complementary to the upstream and downstream sequences bracketing said region.

6. (original): The method of claim 1, wherein said target nucleic acid is double-stranded and said first and second oligomers form triplexes with said upstream and downstream sequences bracketing said region.

7. (original): The method of claim 1, which is performed simultaneously on a multiplicity of target nucleic acids using a multiplicity of identification probes having particulate labels of differing hues coupled to oligomers comprising sequences complementary to a multiplicity of said upstream and downstream sequences bracketing a multiplicity of such regions.

8. (previously presented): A method to detect the presence of a target nucleic acid of known sequence, which method comprises

contacting a sample to be tested for containing said target nucleic acid and further containing non-target nucleic acid with at least first and second probes that bracket a region of said target nucleic acid, which first probe comprises a first oligomer specific for a sequence upstream of said region coupled to a first particulate label and said second probe comprises a second oligomer specific for a proximal sequence downstream of said region coupled to a second particulate label;

wherein said first and second particulate labels are observable by microscopy, and

observing by microscopy the presence or absence of proximity of the first and second particulate labels to each other, whereby the presence of said proximity indicates the presence of said target nucleic acid,

wherein said method does not include a step of separating the target nucleic acid from non-target nucleic acid.

9. (previously presented): The method of claim 8, wherein said first and second particulate labels comprise first and second fluorophores.

10. (previously presented): The method of claim 9, wherein said first and second fluorophores are the same as each other.

11. (original): The method of claim 8, wherein said first and second oligomers are peptide nucleic acids.

12. (original): The method of claim 8, wherein said target nucleic acid is single-stranded and said first and second oligomers are complementary to the upstream and downstream sequences bracketing said region.

13. (original): The method of claim 8, wherein said target nucleic acid is double-stranded and said first and second oligomers form triplexes with said upstream and downstream sequences bracketing said region.

14. (original): The method of claim 8, which is performed simultaneously on a multiplicity of target nucleic acids, using a multiplicity of identification probes having particulate labels of differing hues for each known sequence targeted coupled to oligomers with different specificities according to the sequences targeted.

15. (original): The method of claim 8, wherein said target nucleic acid of known sequence is derived from an organism.

16. (original): The method of claim 15, wherein the organism is an infectious agent.

17. (original): The method of claim 15, wherein the organism is a human subject.

18-47. (canceled)